16(745

Schreiber, David

From:

Sent:

Foley, Shanon Tuesday, August 02, 2005 8:04 AM Schreiber, David

To:

Subject:

10/808964

Hi David. Please search nt SEQ ID NO: 2 and its complement. Please also include an interference search.

Thank you. Shanon

(Otqsu) Anola Blank (uspto)

.

OM nucleic

Run on:

Sequence:

Minimum DB Maximum DB

Database

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Direct Submission

Submitted (11-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EWRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Geoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial BCORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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CO413933 ESTB4431B
CV136509 ESTB471B
CV141605 ESTB471B
CV141400 ESTB451004
CV133795 ESTB4103
CV133994 ESTB4103
CV141902 ESTB41139
CV141902 ESTB51203
CV141902 ESTB51203
CV141480 ESTB5248
CV141069 ESTB5227B
CV141069 ESTB4492
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AERCA8FE19 of RPCI-98 library from Drosophila melanogaster (fruit genomic survey sequence.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
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Pred. No. 0.00037;
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CV139795
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/note="end : TET3"
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KEYWORDS
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Compugen Ltd
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                                             GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
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9b htc:.*

9b est2:.*

9b est4:..*

9b est4:..*

9b est6:..*

9b gs8:..*
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Perfect score:
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GA Ba0028F15f Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum carboreum cBNA clone GA Ba0028F15f, mRNA sequence.
                                                                                                                                                                                                                                                         1401 TACAATCCCCCAACCCTTCTCCTACCACTCCCGTTACTTCACACCCCAAACCTGTTGTTGA 1460
                                                                                                                                                                                                                                                                                                                                                     1461 CTCCACCATTGATTACTTCCAACCAAATAACAAAAGGAATCAGCTTTGGATGAGGCTACA 1520
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                                                                                                                                                                                            Gossýpium arboreum
bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Malvales, Malvaceae, Malvoideae, Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 870)
Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J.,
Wing,R.A., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution
of the cotton fiber
Unpublished (2000)
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/tissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/note="Vector: pBK-CMV; Site_l: BcoRI; Site_2: XhoI"
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                                                     2.8%; Score 50.2; DB 9; 1
16.5%; Pred. No. 0.023;
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4293
Pax: 864 656 4293
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/organia="Gossypium arboreum"
/mol_type="mRNA"
/strain="AKA"
                                                                                                                  Conservative 120; Mismatches
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Seq primer: TAATACGACTCACTATAGGG
High quality sequence start: 6
High quality sequence stop: 659.
Location/Qualifiers
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/db_xref="taxon:29729"
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/note="end : TET3"
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Submitted (02-UN-1999) Genoscope - Centre National de Sequencage :
Bp 1919 19106E SYRX cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
- Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcokI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://dpcpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 919 bp DNA linear GSS 04-JUN-1999 DrackRefile melanogaster genome survey sequence TET3 end of BAC # BACRZ6fil6 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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                                              1327 ATTCTAGATGATAACTTTGTAACAAAGGCCACAGCCCTAACCTATGACCCATATGTAAAC 1386
                                                                                                                                             1387 TACTCCTCCCGCCATACAATCCCCCAACCCTTCTCCTACCACTCCCGTTACTTCACACCC 1446
                                                                                                                                                                                                                                        1507 TGGATGAGGCTACAAACCTCTAGAAATGTGGACCACGTAGGCCTCGGCACTGCGTTCGAA 1566
                                                                                                                                                                                                                                                                                                                                                                                                                               1627 TTTAATCTTAAAGACCCCCCCCTTAAACCCTAAATGAATAAAAATAAAAACCATTACGAT 1686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 939)
    Gaps
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  Conservative 138; Mismatches 178; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              604 TWAMMTAAWAAAAAWATTAAAAAWTTWTTWTTAMTTAMTAMAW 562
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mol type="genomic DNA"
db xref="taxon:7227"
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/clone="BACR26H16"
/clone_lib="RPCI-98"
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EtESTef53d09.yl Elmeria tenella M5-6 Excised CDNA Elmeria tenella
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                                                                                                  1054 CGCCACCGCTACCGTTGGAGGAAAATGGCATCTTCAACACCCGCCTCTCCCGCACC 1113
                                                                                                                                                                                                                                                                                                                                                                              Sukaryota; Alveolata; Apicomplexa; Coccidia; Bimeriida; Bimeriidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
Contact David Sibley (toxoest@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Seg primer: -40RP from Gibco.
                                                                       508
                                                                                                                             1 (bases 1 to 573)
Liberator, P., Diaz, C., Tang, K., Marra, M., Hillier, L., Kucaba, T., Martin, J., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Perevs, S., Saaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, B., Köhn, S., Florence, N., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., Wilson, R. and
                                           994 CACCGCCCCCCCAGCCATCTTGGCCAGATCCTCCGCCGCCGCCCCTGGCTCGTCCACCCC
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WashU-Merck Eimeria tenella project Unpublished (1999)
Contact: David Sibley, Ph.D.
WashU-Merck Eimeria tenella project
WashU-Merck Eimeria tenella project
WashIngton University School of Medicine
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                           TTCGGATATACTGTCAAGGCTACCACAGTCAGAACGCCCTCCTGGGC 1160
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 48.5%; Pred. No. 0.063;
iive 0; Mismatches 86; Indels
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               81; Conservative
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Best Local Similarity
Matches 81; Conserv
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Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi, Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@georriken.jp, URL:http://hgp.georriken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                       ö
                                                                                                                                                                                                                                                                                                                         AG365778 1141 bp DNA linear GSS 03-JUN-2004 mus musculus molossinus DNA, clone:MSMg01-168K18.TJ, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institude, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
                                                                                                                                                           294 gadargeageageagerecercarearrecirirreagegraderrecergeagradea 353
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                  980 ACCGCAGAAGAAGACACCGCCCCCGCAGCCATCTTGGCCAGATCCTCCGCCGCCGCCCCT
                                                                                                                                                                                                                                                                       354 GCAGCAGCAGCCACAGCCACAGCCGCCGCCCCCTGTCCCAACAGCAGCAGCAGTCGCG
                                                                                                            920 GTAATACTACAGCAGCGCACTTCTTTCACTTTTATAGGATGACGTATCCAAGGAGGCGTT
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Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
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BAC end Sequences of Library MSMg01
Unpublished
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Score 48.2; DB 6; Length 573; Pred. No. 0.074; 0; Mismatches 93; Indels
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/clone_lib="MSMg01 Mouse Male BAC Library"
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35.2%; Pred. No. 0.13;
tive 0; Mismatches 175;
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/sub_species="molossinus"
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/clone="MSMg01-168K18.TJ"
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GSS.
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Mus musculus molossinus
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: EcoRI
2.7%;
ilarity 52.8%;
Conservative 0
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Matches 95; Conservative
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S71 bp mRNA linear EST 26-NOV-2002 wialc.pk003.e22 s' end, mRNA sequence.
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                                                                    1415 CCTTCTCCTACCACTCCCGTTACTTCACACACAAACCTGTTCTTGACTCCACCATTGATT 1474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
XhoI; Wheat (Triticum aestivum, Hi Line) immature anthers"
                                                                                                                                                                                                           1475 ACTTCCAACCAAATAACAAAAGGAATCAGCTTTGGATGAGGCTACAAACCTCTAGAAATG 1534
                                                                                                                                                                                                                                                   : | |: | |:: | |:| |:: | |:: | |:: | |:: | |:: | |:: | |:: | | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |: | |:: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |:
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z., Miao, G., Caraher, N. and Hanafey, M.K.
DuPont Wheat cDNA Sequence
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1515 CCTAAATGAATAAAATAAAAACCATTACGATGTGATAACAAAAAAGACTCAGTAA 1710
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E. I DuPont de Nemours and Company
E. I DuPont de Nemours and Company
Tel: 302-631-2607
Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
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Pred. No. 0.21;
0; Mismatches
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/db_xref="taxon:4565"
/clone="wialc.pk003.e22"
/tissue type="anthers"
/lab_host="DH108"
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- Web: www.genoscope.cns.fr)
- Determination of this BAC-end sequence was carried out as part of a collaboration with the Barkeley Droscophila Genome Project (BDGP). The BDGP is constructing a physical map of the Droscophila melanogaster genome using these BACs. For further information please see http://www.fruifily.org The BDGP Droscophila melanogaster BAC library was prepared by Kazutcyo Googawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-99 and was constructed by partial EcoRI digestion of Droscophila DNA provided by the BDGP from the isogenic strain v2: cn bw sp, the same strain used for the BDGP's pl and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/droscophila_bac.htm.
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACN14D09 of RPCI-98 library from Drosophila melanogaster (fruit
AL066784
AL066784.1 GI:4945247
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                                                                                                                                                                                 CGCCACCGCTACCGTTGGAGAAGGAAAATGGCATCTTCAACACCCGCCTCTCCCGCACC
                                       CACCGCCCCCGCAGCCATCTTGGCCAGATCCTCCGCCGCCGCCCCTGGCTCGTCCACCCC 1053
                                                                                                     552 NANNCCCNCNANANANANACHNICHNINANACHNINANANACHNINANANACHTTTT
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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|mol_type="genomic DNA"
|db_xref="taxon:7227"
|clone="BACR14D09"
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/note="end : TET3"
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1 (bases 1 to 857)

2 Uenishi, H., Eguchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H., PRDE (Fig) EST Date Arghorer): construction of a database for ESTs derived from porcine full-length cDNA libraries

1 Nucleic Acids Res. 32 (1), D484-D488 (2004)

1 Contact: Hirohide Uenishi
Animal Genome Laboratory, Genome Research Department
Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
Fax: +81-29-838-8627
Email: huenishi@affrc.go.jp
EST project with full-length enriched cDNA libraries carried out in Animal Genome Research Program (Japan) by National Institute of Agrobiological Sciences and STAPF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
                                                                                                                                                           BP162319 11-length enriched swine cDNA linear EST 30-DEC-2003 BP162319 full-length enriched swine cDNA library, adult thymus Sus scrofa cDNA clone THY010093C05 5', mRNA sequence.
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/dev_stage="adult"
/clone_lib="full-length enriched swine cDNA library, adult
thymus"
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quality bases were trimmed based on the quality values.
Location/Qualifiers
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57.0%; Pred. No. 0.23;
ive 0; Mismatches 64; Indels
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/db_xref="taxon:9823"
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Best Local Similarity 57.0
Matches 85; Conservative
                                                                                                                                                                                                                                                                                      Sus scrofa (pig)
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CNSOOJTL 909 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR39G08 of RPCI-98 library from Drosophila melanogaster (fruit

LOCUS

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Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the Berkelsy Drosophila denome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-99 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and box to order individual BAC clones, the entire library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                            Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 BVRY cedex - FRANCE (B-mail : segref@genoscope.cns.fr
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Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta, Pterygota;
Meoptera, Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="texon:7227"
/clone="BACR39G08"
/clone=lib="RPCI-98"
/note="end : TET3"
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ilarity 22.6%; Pred. No. 0.23;
Conservative 118; Mismatches 190;
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AL076720.1 GI:4956298
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Mentha x piperita (peppermint)
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Email: lange-m@mail.wsu.edu.
Location/Qualifiers
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                   AW255252.1 GI:7244504
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//clone_lib="FL4"
//clone_long); Vector: pSport1; Site_1: Sal1; Site_2: NotI;
(20cm-long); Vector: pSport1; Site_1: Sal1; Site_2: NotI;
An unidirectional cDNA library generated from [Developed inflorescence and rachis (20cm-long)]. cDNA was prepared from poly4+ mRNA using SuperScript Plasmid System Kit (Invircem). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
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                                                                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta,
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
                                         CA222795 560 bp mRNA linear EST 25-SEP-2003
SCEZFL4038H05.g FL4 Saccharum officinarum cDNA clone SCEZFL4038H05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 038 row: H column: 05
Seq primer: T7 Promoter Primer.
Location/Qualifiers
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Vettore, A.L., da Silva, F.R., Kemper, B.L. and Arruda, P. The libraries that made SUCEST
Genet. Nol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
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                                                                                                                                                                                                                                                                                                                                                                                            Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Gaixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Saccharum officinarum"
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clone="SCEZFL4038H05"
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                                                                                                                                                                                          Saccharum officinarum
                                                                                5', mRNA sequence.
CA222795
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Enkaryota; Viridiplantae; Streptophyta; Enkaryota; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. B. (Bases 1 to 460)
Sequencing of ESTs from loblolly pine embryonic libraries
Unpublished (2004)
Contact: C. Robin Buell
Plant Genomics Group
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: rbuell@tigr.org
This clone is available through TIGR. Please contact pine@tigr.org
for further information
                                                                                                                                                                                                                                                                   evaluation of expressed sequence tags from mint glandular trichomes Proc. Natl. Acad. Sci. U.S.A. 97 (6), 2934-2939 (2000)
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EST855400 Sequencing EST8 from loblolly pine embryos Pinus taeda CDNA clone RPID242 5' end, mRNA sequence.
                                                                                                                                                                                   1 (bases 1 to 401)
Lange, B.M., Wildung, M.R., Stauber, B.J., Sanchez, C., Pouchnik, D. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          959 TGACGTATCCAAGGAGGCGTTACCGCAGAAGAAGACACCGCCCCCCGCAGCCATCTTGGCC 1018
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Mentha x piperita
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spernatophyta, Magnoliophyta, eudicotyledons, core eudicots,
asterids, lamiids, Lamiales, Lamiaceae, Nepetoideae, Nepeteae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Lange, B.M.
Institute of Biological Chemistry/Washington State University
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/cell type="secretory"
/clone_lib="peppermint glandular trichome"
/note="vector: lamba ZAPII"
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Best Local Similarity 55.7%; Pred. No. 0.28;
Matches 88; Conservative 0; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1079 AAAATGGCATCTTCAACACCCGCCTCTCCCGCACCTTC 1116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
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/db_xref="taxon:34256"
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SOURCE
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CV137364/c
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DEFINITION
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AUTHORS
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/(lone="RPID242"
/(lab_host="E.coli DH10B-TonA"
/(clone=lib="Sequencing RSTB from loblolly pine embryos"
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Embryo; Vector: pcMV-SPORT 6.1; Site_1: Not1; Site_2:
ECRY; tissue: Whole megagametophytes isolated from pine
seeds Whole embryos excised from these megagametophytes,
whole somatic embryos excised from these megagametophytes,
whole somatic embryos excised from these megagametophytes,
sused for library construction. Pine cones were harvested
weekly from open-pollinated 7.56 mother trees, collections
occurred from 7/01/02 until 10/15/02. Whole
megagametophytes were first isolated from pine seeds, and
whole embryos excised from these megagametophytes each was
flash frozen. Embryo development was assessed using the
system of Pullman et al (Pullman GS, Johnson S, Peter G,
Cairney J, Xu N. 2003. Loblolly Pine somatic
embryogenesis development of a maturation medium and
resulting embryo quality. Plant Cell Reports 21:747-758
(http://link.springer.de/link/service/journals/00299/conte
nts/03100586/). Por photographs see Clavatta et al 2001.
(Clavatta VT, Morillon R, Pullman GS, Chrispeels M,
Cairney J. 2001. An aquaglyceroporin is abundantly
expressed early in the development of the suspensor and
the embryo proper of loblolly pine (Pinus taeda L.). Plant
Physiol. 127: 1556-1567

(http://www.plantphysiol.org/cgi/content/full/127/4/1556))
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Buell, C.R., Haiao, J. and Cairney, J. Sequencing of ESTs from loblolly pine embryonic libraries
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                                                                                                       /mol_type="mRNA"
/culfivar="7-5 mother tree, open-pollinated tree from,
yons, Georgia, USA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.5%; Score 45.2; DB 7; Length 460; 68.9%; Pred. No. 0.49; ive 0; Mismatches 28; Indels (
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The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
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Seg primer: ATT TAG GTG ACA CTA TAG.
                                                                                'organism="Pinus taeda"
                       socation/Qualifiers
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Contact: C. Robin Buell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 68.99
Matches 62, Conservative
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AUTHORS
TITLE
JOURNAL
COMMENT
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/lab hose="RIBLED" Coli DH10B-TonA"
/clone lib="Requencing ESTS from lobiolly pine embryos"
/clone lib="Sequencing ESTS from lobiolly pine embryos"
/clone lib="Sequencing ESTS from lobiolly pine embryos"
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EGORY, tisue: Whole embryos excised from these megagametophytes, whole embryos excised from these megagametophytes, whole embryos, megagametophytes, and somatic embryos was used for library construction. Pine conse were harvested weekly from open-pollinated 7-56 mother trees, collections occurred from 7/01/02 until 10/15/02. Whole megagametophytes were first isolated from pine seeds, and whole embryos excised from these megagametophytes each was flash frozen. Embryo development was assessed using the system of Pullman et al (Pullman GS, Johnson S, Peter G. Cairney J, Xu N. 2003. Lobiolly pine somatic embryogenesis: development of a maturation medium and resulting embryo quality. Plant Cell Reports 21:747-758 (http://libr.springer.de/libr/Rervice/journals/00299/contents/03/00586/). For photographs see Ciavatta et al 2001. (Ciavatta VT, Morillon R, Pullman GS, Chrispeels M, Cairney J. 2001. An aquaglyceroporin is abundantly expressed early in the development of the suspensor and the embryo proper of lobiolly pine (Pinus taeda L.). Plant Physiol. 127: 1556-1567
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Buell, C.R., Haiso, J. and Cairney, J.
Sequencing of ESTs from loblolly pine embryonic libraries
Conteat: C. Robin Buell
Plant Genomics Group
This clone is available through TIGR. Please contact pine@tigr.org for further information.
Location/Qualifiers
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/cultivar="7-56 mother tree, open-pollinated tree from,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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9712 Medical Center Dr, Rockville, MD 20850, USA
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                                                                                                                                              organism="Pinus taeda"
                                                                                                                                                                                                                                                Lyons, Georgia, USA"
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Best Local Similarity 68.9
Matches 62; Conservative
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Job time : 5981 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        current in the real filter Also and somatic embryos was used for library construction. Pine cones were harvested weekly from open-pollinated 7-56 mother trees, collections occurred from 7/0/102 until 10/15/02. Whole concurred from 7/0/102 until 10/15/02. Whole megagametophytes were first isolated from pine seeds, and whole embryos excised from these megagametophytes accided from these megagametophytes accided from these megagametophytes accided was flash frozen. Embryo development was assessed using the system of Pullman et al (Pullman GS, Johnson S, Peter G, Cairney J, Xu N. 2003. Loblolly Pine somatic embryogenesis development for amaturation medium and resulting embryo development for amaturation medium and resulting embryo quality. Plant Cell Reports 21:747-758 (http://link.springer.de/link/service/journals/00299/contents/03/00586/). For photographs see Ciavatta et al 2001. (Ciavatta VT, Norillon R, Pullman GS, Chrispeels M, Cairney J. 2001. An aquaglyceroporin is abundantly expressed early in the development of the suspensor and the embryo proper of loblolly pine (Pinus taeda L). Plant Physiol. 127: 1556-1567
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(http://www.plantphysiol.org/cgi/content/full/127/4/1556))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="Sequencing ESTB from loblolly pine embryos" /note="Organ: Zygotic Embryo and Megagametophyte, Somatic Embryo; Vector: pCMV-SPORT 6.1; Site 1: Not1; Site 2: EcoRV; tissue: Whole megagametophytes isolated from pine seeds, Whole embryos excised from these megagametophytes, whole somatic embryos and suspensor tissue from tissue culture, isolated from cell line Al2. Pooled RNA from
Email: rbuell@tigr.org
This clone is available through TIGR. Please contact pine@tigr.org
for further information
Seg primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
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Buell, C.R., Heiao, J. and Cairney, J. Sequencing of ESTs from loblolly pine embryonic libraries
                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
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Lyons, Georgia, USA"
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68.9%; Pred. No. 0.53;
ive 0; Mismatches 28; Indels
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                                                                                                                                                                                                                                                                                                             organism="Pinus taeda"
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Contact: C. Robin Buell
Plant Genomics Group
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Best Local Similarity 68.9
Matches 62; Conservative
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/clone="RRIBATO"
//clone="RRIBATO"
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Embryo; Vector: pCMV-SPORT 6.1; Site 1: Not1; Site 2:
Embryo; Vector: pCMV-SPORT 6.1; Site 1: Not1; Site 2:
ERORN; tissue: Whole megagametophytes isolated from pine
seeds, Whole embryos excised from these megagametophytes,
whole somatic embryos and suspensor tissue from tissue
culture, isolated from call line Al2. Pooled RNA from
zygotic embryos, megagametophytes, and somatic embryos was
used for library construction. Pine conse were harvested
weekly from open-pollinated 7-56 mother trees, collections
occurred from 7/01/02 until 10/15/02. Whole
megagametophytes were first isolated from pine seeds, and
whole embryos excised from these megagametophytes ach was
flash frozen. Embryo development was assessed using the
system of Pullman et al (Pullman GS, Johnson S, Peter G,
cairney J, xun v. 2003. Loblolly Pine somatic
embryogenesis: development of a maturation medium and
resulting embryo quality. Plant Cell Reports 21:747-758
(http://link.apringer.de/link/service/journals/00299/conte
nts/03/00586/). For photographs see Ciavatta et al 2001.
(Ciavatta VI, Morillon R, Pullman GS, Chrispeels M,
Cairney J . 2001. An aquaglyceroporin is abundantly
expressed early in the development of the suspensor and
the embryo proper of loblolly pine (Pinus taeda L). Plant
Physiol. 127: 1556-1567
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...
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: rbuell@tigr.org
This clone is available through TIGR. Please contact pine@tigr.org
for further information
Seg primer: ATT TAG GTG ACA CTA TAG.
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/cultivar="7-56 mother tree, open-pollinated tree from,
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
               Copyright
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Run on:

August 4, 2005, 21:48:07; Search time 981 Seconds (without alignments) 10698.982 Million cell updates/sec

US-10-808-964A-2 1773 Title: Perfect score:

1 ggtacctccgtggattgttc.....caaatcggccttcgggtacc 1773 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4390206 seqs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters:

seg length: 0 seg length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

genesequi980s;
genesequi200s;
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genesequi2001as;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aal57177 Porcine c	Abx08205 PMWS-Porc	Abx08203 PMWS-Porc	Abx08207 CT-Porcin	Abx08206 CT-Porcin	Abx08204 PMWS-Porc	Abx08219 PMWS-Porc	Abx08202 PMWS-Porc	Abx08208 CT-Porcin	Abx08220 PK-15-Por	Aah74867 Nucleotid	Abx94361 Rolling c	Aah74865 Nucleotid	Abx94355 Rolling c	Aah74866 Nucleotid	Abx94356 Rolling c	Aaf75839 DNA fragm	Aal57176 Porcine c	Aax35013 Nucvleoti	Aaf28320 pJP107 do
SUMMARIES	a a	AAL57177	ABX08205	ABX08203	ABX08207	ABX08206	ABX08204	ABX08219	ABX08202	ABX08208	ABX08220	AAH74867	ABX94361	AAH74865	ABX94355	AAH74866	ABX94356	AAF75839	AAL57176	AAX35013	AAF28320
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	& Query Match	100.0	72.5	72.1	72.0	71.9	71.9	71.7	70.6	68.7	68.3	67.5	67.5	67.4	67.4	67.4	67.4	59.8	59.7	59.5	59.4
•	Score	1773	1285.2	1278.8	1277.2	1274	1274	1270.8	1252	1218.2	1210.2	1196.8	1196.8	1195.8	1195.8	1195.8	1195.8	1059.8	1058.4	1055.6	1053.2
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ALIGNMENTS

Porcine circovirus type 2, PCV1-2; PCV1; PMWS; weaning piglet; dyspnoea; progressive weight loss; postweaning multisystemic wasting syndrome; ds; tachypnea; anaemia; diarrhoea; jaundice; virucide; vaccine; PCV2; gene; viral infection; chimeric. Porcine circovirus type 1-2 chimeric DNA. AAL57177 standard; DNA; 1773 BP. (revised)
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Porcine circovirus type 1. Porcine circovirus type 2. Chimeric.

Location/Qualifiers 958. .1659 /*tag= a /product= "Porcine circovirus type 2 ORP2 capsid protein" WO2003049703-A2

11-DEC-2002; 2002WO-US039646. 19-JUN-2003.

12-DEC-2001; 2001US-0340775P. 08-NOV-2002; 2002US-0424340P. 09-DEC-2002; 2002US-00314512.

(VIRG) VIRGINIA TECH INTELLECTUAL PROPERTIES. (IOWA) UNIV IOWA STATE RES FOUND INC.

Meng X, Fenaux M, Halbur PG;

WPI; 2003-513959/48. P-PSDB; AAO23063.

circovirus, infection and/or New infectious chimeric nucleic acid molecule of porcine useful for preventing and/or treating pigs against viral postweaning multisystemic wasting syndrome. New infectious chimeric useful for preventing an

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9; 85pp; English 13; Fig The invention relates to a novel infectious chimeric nucleic acid molecule of porcine circovirus (PCV1-2) which comprises a nucleic acid encoding an infectious, non-pathogenic PCV1 (porcine circovirus type 1) containing an immunogenic open reading frame (ORF) gene of a pathogenic containing an immunogenic open reading frame (ORF) gene of a pathogenic provide circovirus type 2) in place of a PCV1 ORF gene. Postweaning multisystemic wasting syndrome (PMMS) is a complex disease of weaning piglets that is becoming increasingly more widespread. The condition poses a potentially serious economic threat to the swine industry, thus causative agent of PMMS. PWMS mainly affects pigs between 5-18 weeks of causative agent of PMMS. PWMS mainly affects pigs between 5-18 weeks of age and clinical symptoms include progressive weight loss, dyspnoea, tachypnea, anaemia, diarrhoea and jaundice. The chimeric polynucleotide of the invention demonstrates virucide activity and may be utilised as a vaccine for PMMS. The methods and compositions of the present invention may be useful for the prevention and/or treatment of pigs against viral infection and/or PMMS. The current sequence is that of the PCV1-2.

Sequence 1773 BP; 472 A; 511 C; 359 G; 431 T; 0 U; 0 Other;

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540 540 999 120 180 240 240 360 360 420 420 480 480 600 900 9 9 TCTTTATTCTGCTGGTCGGTTCCTTTCGCTTTTCTCGATGTGGCAGCGGGCACCAAAATAC TAGAGAGCTTCTACAGCTGGGACAGCTGAGGAGTACCATTCCTGGGGGGCCTGATTG CTGGTAATCAAAATACTGCGGGCCAAAAAGGAACAGTACCCCCTTTAGTCTCTACAGTC GGGCCCACTATGACGTGTACAGCTGTTCCAATCACGCTGCTGCATCTTCCCGCTCACT TTCAAAAGTTCAGCCAGCCGGGGAAATTTCTCACATACGTTACAGGAAACTGCTCGGCT GGTACCTCCGTGGATTGTTCTCCAGCAGTCTTCCAAAATTGCAAAGTAGTAATCCTCCGA GGTACCTCCGTGGATTGTTCTCCAGCAGTCTTCCAAAATTGCAAAGTAGTAATCCTCCGA TAGAGAGCTTCTACAGCTGGGACAGCAGTTGAGGAGTACCATTCCTGGGGGGCCTGATTG CTGGTAATCAAAATACTGCGGGCCAAAAAAGGAACAGTACCCCCTTTAGTCTCTACAGTC AATGGATACCGGTCACACAGTCTCAGTAGATCATCCCAAGGTAACCAGCCATAAAATCA TCCAAAACAACAACTTCTTCTCCATGATATCCATCCCACCACTTATTTCTACTAGGCTTC TACGGGCCCACTGGCTCTTCCCACAACCGGGC TACGGGCCCACTGGCTCTTCCCACAACCGGGC GGGCCCACTATGACGTGTACAGCTGTCTTCCAATCACGCTGCTGCTTCTTCCCGCTCACT Trcadadagricagecageeegeaaarricicacatacgriacaggaactgeregeer ACAGTCACCAAAAGACCCCGTCTCCAAAAGGGTACTCACAGCAGTAGACAGGTCGCTGCGC STATGTGGCCTTCTTTACTGCAGTAT Gaps ö 9; Length 1773; 0; Indels B Query Match 100.0%; Score 1773; Best Local Similarity 100.0%; Pred. No. 0; Matches 1773; Conservative 0; Mismatches CAGTAGGTGTCCCTAGGCTCAGCAAAA cagradererectradecreadeaaag 61 181 481 61 121 121 181 241 241 301 301 361 361 421 421 481 541 601

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New porcine circovirus (PCV) nucleic acids for use as a component of vaccines for treating or preventing congenital tremors in pigs.
                                                                                                                       Porcine circovirus genome; PCV; vaccine; type I PCV strain; type II PCV strain; congenital tremor; pig; whole PCV vaccine; passive immunisation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1768 BP; 453 A; 358 C; 493 G; 464 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                             Kanitz CL;
GGGTCCACTGCTTCAAATCGGCCTTCGGGTACC 1773
       1741 GGGTCCACTGCTTCAAATCGGCCTTCGGGTACC 1773
                                                                                                                                                                                                                                                             Kiupel M,
                                                                                                         PMWS-Porcine circovirus (PCV) P4 genome.
                                                                                                                                                                                                                                                            Choi J,
                                                        BP
                                                                                                                                                                                                                                                                                                                      Claim 1; Page 84; 88pp; English.
                                                        ABX08205 standard; DNA; 1768
                                                                                                                                                                                                           15-JUN-2001; 2001WO-US019220.
                                                                                                                                                                                                                           15-JUN-2000; 2000US-0211710P.
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                                                                                                                                                                                                                                                             Mittal SK, Stevenson GW,
                                                                                                                                                                                                                                            (PURD ) PURDUE RES FOUND
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                                                                                                                                                          Porcine circovirus
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The invention describes an isolated mucleic acid (I) from a porcine circovirus (PCV) where (I) comprises a sequence coding for a circovirus colypeptide. A vaccine comprising a PCV nucleic acid that encodes an immunogenic polypeptide of type I or type II PCV strain and a carrier, is useful for treating or preventing congenital tremors in a pig or its progeny (PCV type I is composed of PK-15-PCV and CT-PCV-P7; PCV type II is composed of PK-15-PCV and CT-PCV-P7; PCV type II is composed of PWMS-PCV-P1, PWMS-PCV-P2, -P3, -P4, and CT-PCV-P5, -P6).

An isolated PCV strain (II) is useful for diagnosing a pathological cause of congenital tremors in a pig which involves determining whether the pig has been infected by PCV strain type I or type II. The determination of the infection is effected by detecting the presence of a PCV nucleic acid in a biological sample from the pig, by detecting hybridisation of an olypeptide in a biological sample from the pig by detecting the presence of PCV polypeptide in a biological sample from the pig by detecting the presence of antibodies directed against a PCV polypeptide in a biological sample of the pig. An expression vector (III) encoding a netting the presence of antibodies directed against congenital tremors.

(II) along with a suitable adjuvant is useful as a whole PCV vaccine, while the antigenic PCV polypeptides are used as components of subunit vaccines. immunisation strategies. This sequence represents a porcine circovirus

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                                                        135 ACTGCGGGCCAAAAAAGGAACAGTACCCCCTTTAGTCTCTACAGTCAATGGATACCGGTC 194
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Score 1285.2; DB 6; Length Pred. No. 0; 0; Mismatches 158; Indels

72.5%; 89.0%;

Matches 1462; Conservative

Similarity

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N-PSDB; ABU02903, ABU02914, ABU02918, ABU02925, ABU02934, ABU02937,
ABU02944, ABU02951, ABU02962, ABU02967.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Porcine circovirus genome; PCV; vaccine; type I PCV strain; type II PCV strain; congenital tremor; pig; whole PCV vaccine; passive immunisation; ds.
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The invention describes an isolated nucleic acid (I) from a porcine circovirus (PCV) where (I) comprises a sequence coding for a circovirus (CC circovirus (PCV) where (I) comprising a PCV nucleic acid that encodes an immunogenic polypeptide of type I or type II PCV strain and a carrier, is useful for treating or preventing congenital tremors in a pig or its progeny (PCV type I is composed of PK-15-PCV and CT-PCV-P7; PCV type II or composed of PMMS-PCV-P1, PMMS-PCV-P2, -P3, -P4, and CT-PCV-P5, -P6).

An isolated PCV strain (II) is useful for diagnosing a pathological cause of congenital tremors in a pig which involves determining whether the pig CC has been infected by PCV strain type I or type II. The determination of the infection is effected by detecting the presence of a PCV nucleic acid in a biological sample from the pig, by detecting hybridisation of an oligomucleotide. Optionally, the determination of infection is effected by detecting the presence of antibody that specifically binds a PCV polypeptide in a biological sample from the pig by detecting the presence of antibody that specifically binds a PCV polypeptide is useful as a vector vaccine against congenital tremore. CC (II) along with a suitable adjuvant is useful as a whole PCV vaccine, while the antigenic PCV polypeptidees are usef as components of subunit confinents at unitabedies against PCV proteins are useful in passive cimmunisation strategies. This sequence represents a porcine circovirus
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Pred. No. 0;
0; Mismatches 162;
Page 83; 88pp; English
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Matches 1458;
Claim 1;
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The invention describes an isolated mucleic acid (I) from a porcine circovirus (PCV) where (I) comprises a sequence coding for a circovirus (C) circovirus (PCV) where (I) comprises a sequence coding for a circovirus (C) delegated by a vaccine comprishing a PCV nucleic acid that enacodes an immunogenic polypeptide of type Ior type II PCV strain and a carrier, is progeny (PCV type I is composed of PW-15-PCV and CT-PCV-P7; PCV type II is composed of PMS-PCV-P1, PWMS-PCV-P2, -P3, -P4, and CT-PCV-P5, -P6).

Can isolated PCV strain (II) is useful for diagnosing a pathological cause of congenital tremors in a pig which involves determining whether the pig CC has been infected by PCV strain type I or type II. The determination of the infection is effected by detecting the presence of PCV polypeptide in a biological sample from the pig, by detecting hybridisation of an oligomucleotide. Optionally, the determination of infection is effected by detecting the presence of antibody that specifically binds a PCV polypeptide of the pig and antibody that specifically binds a PCV polypeptide is useful as a vector vaccine against congenital tremore. CC (II) along with a suitable adjuvant is useful as a whole PCV vaccine, while the antigenic PCV polypeptides as components of subunit conscines. Antibodies against FCV proteins are used as components of subunit communisation strategies. This sequence represents a porcine circovirus
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ABU02948, ABU02955, ABU02960, ABU02966, ABU02968.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New porcine circovirus (PCV) nucleic acids for use as a component vaccines for treating or preventing congenital tremors in pigs.
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                                                                                                                                                                                                      circovirus genome; PCV, vaccine; type I PCV strain; PCV strain; congenital tremor; pig; whole PCV vaccine;
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                                                                                                                                                                 CT-Porcine circovirus (PCV) P6 genome
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Query Match
Best Local Similarity 88.7%;
Matches 1457; Conservative (
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1382 TAAACTACTCCTCCCGCCATACAATCCCCCAACCCTTCTCCTACCACCCGTTACTTCA
                                                                                                                       AGCTTTGGCTGAGGCTACAAACCTCTAGAAATGTGGACCACGTAGGCCTCGGCACTGCGT
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N-PSDB; ABU02905, ABU02912, ABU02921, ABU02928, ABU02933, ABU02940,
ABU02947, ABU02954, ABU02961, ABU02964, ABU02972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Porcine circovirus genome; PCV; vaccine; type I PCV strain; type II PCV strain; congenital tremor; pig; whole PCV vaccine; passive immunisation; ds.
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The invention describes an isolated nucleic acid (I) from a porcine circovirus (PCV) where (I) comprises a sequence coding for a circovirus (CC circovirus (PCV) where (I) comprising a PCV nucleic acid that encodes an immunogenic polypeptide of type I or type II PCV strain and a carrier, is progeny (PCV type I is composed of PK-15-PCV and CT-PCV-P7; PCV type II is composed of PMMS-PCV-P2; PP3, -P4, and CT-PCV-P5, -P6).

An isolated PCV strain (II) is useful for diagnosing a pathological cause of congenital tremors in a pig which involves determining whether the pig has been infected by PCV strain type I or type II. The determination of the infection is effected by detecting the presence of a PCV nucleic acid in a biological sample from the pig, by detecting hybridisation of an oligomical sample from the pig by detecting the presence of PCV polypeptide in a biological sample from the pig by detecting binding of an antibody that specifically binds a PCV colympatide. Optionally, the determination of infection is effected by detecting the presence of antibodies directed against a PCV polypeptide in a biological sample of the pig. An expression vector (III) encoding a PCV polypeptide is useful as a vector vaccine against congenital tremors. (II) along with a sultable adjuvant is useful as a whole PCV vaccine, while the antigenic PCV polypeptides are useful as a whole PCV vaccine, while the antigenic PCV protesing are useful as a whole PCV vaccine.
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Sequence 1768 BP; 451 A; 361 C; 497 G; 459 T; 0 U; 0 Other;

1649 1589 1529 1469 1349 1229 1169 CAGCCCGCGGAAATTTCTGACAAACGTTACAGGGTGCTGCTGCAACGGTCACCAGACT 1409 494 434 554 674 ACTGCGGGCCAAAAAAGGTACAGTTCCACCTTTAGTCTCTACAGTCAATGAATATGATC TTCTTCACCATGGTAACCATCCCACCACTTGTTTCTAGGTGGTTTCCAGTATGTGGTTTC CCCGCTCTCCAACAACGTACTCACAGCAGTAGACAGGTCACTCCGTTGTCTTGAGATCG **ACTGCGGGCCAAAAAGGAACAGTACCCCCTTTAGTCTTACAGTCAATGGATACCGGTC** ACACAGICTCAGIAGAICAICCCAAGGIAACCAGCCAIAAAAAICAICCAAAAACAACAAC TTCTTCTCCATGCATCCCACCACTTATTTCTACTAGGCTTCCAGTAGGTGTCCCT AGCCTCAGCAAAATTACGGGCCCACTGGCTCTTCCCACAACCGGGCGGCCCCACTATGAC cesercrecanantraccaeccentracerritaceacaeccaescececaeareae GTGTACAGCTGTCTTCCAATCACGCTGCTGCATCTTCCCCGCTCACTTTCAAAAGTTCAGC eneracarrectricearicacecrirerecarrirececricacrireaaagricaec CAGCCCGCGGAAATTTCTCACATACGTTACAGGAAACTGCTCGGCTACAGTCACCAAAGA CCCCGTCTCCAAAAGGGTACTCACAGCAGTAGACAGGTCGCTGCCTTCCCCTGGTTCCG 1348 AGGAGCTCCACATTCAATAAGTAAGTTGCCTTCTTTACTGCAATATTCTTTATTCTGCTG GTCGGTTCCTTTCGCTTTCTCGATGTGGCGCGCGCCCAAAATACCACTTCACCTTGTT 675 AAAAGTCTGCTTCTTAGCAAAATTCGCAAACCCCTGGAGGTGAGGAGTTCTACCCTCTTC Gaps 22; Score 1274; DB 6; Length 1768; Pred. No. 0; 0; Mismatches 165; Indels 71.9%; Matches 1455; Conservative Similarity 135 195 1708 1648 315 1528 (1768 1588 1468 1408 615 255 375 435 555 495 Query Match Local 8 8 g 8 6 6 6 g Š 8 & ò 8 & 8 8 8 ठ ò 셤

1141 1321 1741 1168 ATTACCCTCCTCGCCAACAATAAATAATCAAATAGGGAGATTGGGAGCTCCCGTATTTT 1109 1021 1081 1201 1261 CTGTTATTCTAGATGATAACTTTGTAACAAGGCCACACAGCCCTAACCTATGACCCATATG 1381 1441 1501 1561 1621 1681 812 692 632 961 932 452 392 272 215 214 ACGAAGTGAT---AAAAAGACTCAGTAATTTATTTCATATGGAAATTCAGGGCATGGGG 158 1108 CTTGCGCTCGTCTTCGGAAGGATTATTCAGCGTGAACACCCCCCCTTTTATGTGTGGTGG CGCTGCCGAAGTGCGCTGGTAATACTACAGCGCGCACTTCTTTCACTTTTATAGGATGA AGGITGAATICIGGCCCTGCTCCCCCATCACCCAGGGTGATAGGGGAGTGGCTCCACTG AGGTTGAATTCTGGCCCTGCTCCCCATCACCCCAGGTGATAGGGGAGTGGGCTCCACTG CTGTTATTCTAGATGATAACTTTGTACCAAAGGCCAATGCCCTAACCTATGACCCATATG TAAACTACTCCTCCCGCCATACAATCCCCCAACCCTTCTCCTACCACTCCCGTTACTTCA 855 GCCGCTT----TTCTTGCTTGGCATTTT----CACTGACGCTGCCGAGGTGCTGC CGTATCCAAGGAGGCGTTACCGCAGAAGAAGACACCGCCCCCGCAGCATCTTGGCCAGA TCCTCCGCCGCCCCCTGGCTCGTCCACCCCCCGCCACCGCTACCGTTGGAGAAAAA récrédededecedentes de la contra del la contra de la contra del ATGGCATCTTCAACACCCGCCTCTCCCGCACCTTCGGATATACTGTCAAGGCTACCACAG 811 ATGGCATCTTCAACACCCGCCTCTCCGCACCTTCGGATATACTGTCAAGCGTACCACAG TCAGAACGCCCTCCTGGGCGGTGGACATGATGAGATTTAATATTGACGACTTTGTTCCCC CGGGAGGGGGACCAACAAATCTCTATACCCTTTGAATACTACAGAATAAGAAAGGTTA TAPACTACTCCTCCGCCGTACAATCCCCCAACCCTTCTCCTACCACTCCGGTTACTTCA GAGAATTTAATCTTAAAGACCCCCCACTTAACCCCTAAATG---AAAAATAAAAACCATT ACGATGTGATAACAAAAAGACTCAGTAATTTATTTTATATGGGAAAAGGGCACAGGGTG AGCTTTGGCTGAGGCTACAAACCTCTAGAAATGTGGACCACGTAGGCCTCGGCACTGCGT GAGAATTTAATCTTAAAGACCCCCCACTTAAACCCTAAATGAATAAAAATAAAAACCATT AGCTTTGGATGAGGCTACAAACCTCTAGAAATGTGGACCACGTAGGCCT GGTCCACTGCTTCAAATCGGCC 1763 GGGAAAGGGTGACGAACTGGCC 136 871 1262 631 1382 1022 1082 391 331 988 962 1142 751 1322 1442 1502 902 1202 1562 1622 1742 931 691 571 511 451 271 g 셤 셤 ઠે 셤 g 셤 셤 ò 8 ò ሯ Š 셤 요 g g 임 ઠે g 요 a à ઠે ò ò ઠે 8 ઠે 8 셤 Š ò

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An isolated PCV strain (II) is useful for diagnosing a pathological cause of congenital tremors in a pig which involves determining whether the pig chas been infected by PCV strain type I or type II. The determination of in a biological sample from the pig, by detecting hybridisation of an oligonucleotide. Optionally, the determination of infection is effected by detecting the presence of PCV polypeptide in a biological sample from the pig by detecting binding of an antibody that specifically binds a PCV polypeptide. Optionally, the determination of infection is effected by detecting the presence of antibodies directed against a PCV polypeptide in a biological sample of the pig. An expression vector (III) encoding a PCV polypeptide is useful as a vector vaccine against congenital tremors. (II) along with a suitable adjuvant is useful as a whole PCV vaccine, while the antigenic PCV polypeptides are used as components of subunit communisation strategies. This sequence represents a porcine circovirus
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N-PSDB; ABU02904, ABU02910, ABU02919, ABU02926, ABU02932, ABU02939,
                                                                                                                                                                                                                                                                                                                                                                                                                         New porcine circovirus (PCV) nucleic acids for use as a component vaccines for treating or preventing congenital tremors in pigs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
                                                                                                          circovirus genome, PCV, vaccine, type I PCV strain, PCV strain; congenital tremor; pig; whole PCV vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1768;
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Pred. No. 0;
0; Mismatches 165; Indels
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                                                                                                                                                                                                                                                                                                                                         Kiupel M,
                                                                                   PMWS-Porcine circovirus (PCV) P3 genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 83-84; 88pp; English.
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ABX08204 standard; DNA; 1768
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Best Local Similarity 88.6%;
Matches 1455; Conservative
                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                         Stevenson GW,
                                                                                                            Porcine circovirus genome
type II PCV strain; conge
passive immunisation; ds.
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                                                                                    CTGTTATTCTAGATGATAACTTTGTAACAAAGGCCACAGCCCTAACCTATGACCCATATG
          CIGTTATTCTAGATGATAACTTTGTACCAAAGGCCAATGCCCTAACCTATGACCCATATG
                                                                                                                                                                GAGAATTTAATCTTAAAGACCCCCCCTTAAACCCTTAAATGAATAAAAATAAAAACCATT
                                                                                                                                                                                                     GAGAATTTAATCTTAAAGACCCCCCACTTAACCCCTAAATG---AAAAATAAAAACCATT
                                                       TAAACTACTCCTCCCCCATACAATCCCCCAACCCTTCTCCTACCACTCCCGTTACTTCA
                                                                                                                AGCTTTGGATGAGGCTACAAACCTCTAGAAATGTGGACCACGTAGGCCTCGGCACTGCGT
                                                                                                                             AGCTTTGGCTGAGGCTACAAACCTCTAGAAATGTGGACCACGTAGGCCTCGGCACTGCGT
                                                                                                                                                    ACGAAGTGAT - - - AAAAAAGACTCAGTAATTTATTTCATATGGAAATTCAGGGCATGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes an isolated nucleic acid (I) from a porcine circovirus (PCV) where (I) comprises a sequence coding for a circovir polypeptide. A vaccine comprising a PCV nucleic acid that encodes an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU02936, ABU02938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New porcine circovirus (PCV) nucleic acids for use as a component vaccines for treating or preventing congenital tremors in pigs.
                                                                                                                                                                                                                                                                                                                                                                                                                 circovirus genome; PCV; vaccine; type I PCV strain; PCV strain; congenital tremor; pig; whole PCV vaccine;
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ABU02946, ABU02953, ABU02959, ABU02969, ABU02971
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                                                                                                                                                                                                                                                                                                                                                                                              PMWS-Porcine circovirus (PCV) genome.
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                                                                                                                                                                                                                                                                                        GGGAAAGGGTGACGAACTGGCC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Choi J,
                                                                                                                                                                                                                                                                                                                                      ABX08219 standard; DNA; 1774 BP
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cc immunogenic polypeptide of type I or type II PCV strain and a carrier, is useful for treating or preventing congenital tremors in a pig or its progeny (PCV type I is composed of PW-15-PCV and CT-PCV-P7, PCV type II is composed of PWMS-PCV-P2, -P3, -P4, and CT-PCV-P5, -P6).

An isolated PCV strain (II) is useful for diagnosing a pathological cause of congenital tremors in a pig which involves determining whether the pig has been infected by PCV strain type I or type II. The determination of the infection is effected by detecting the presence of a PCV nucleic acid in a biological sample from the pig, by detecting hybridisation of an coligonucleotide. Optionally, the determination of infection is effected by detecting the presence of PCV polypeptide in a biological sample from the pig by detecting the presence of PCV polypeptide of infection is effected by detecting the presence of antibodise directed against a PCV polypeptide or a biological sample of the pig. An expression vector (III) encoding a CC pulphoptide is useful as a vector vaccine against congenital tremors. (II) along with a suitable adjuvant is useful as a whole PCV vaccine, while the antigenic PCV pupper are useful in passive in passive in a plantic congenital tremors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunisation strategies. This sequence represents a porcine circovirus
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GTTTTTCTCCTCCTCGGAAGGATTATTAAGGGTGAACACCCCACCTCTTATGGGGTTGCGG

(first entry)

20-JAN-2003

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202/c ABX08202 standard; DNA; 1762 BP.

ABX08202

ABX08202/ ID ABX0 XX AC ABX0

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The invention describes an isolated nucleic acid (1) from a porcine circovirus (PCV) where (I) comprises a sequence coding for a circovirus polypeptide. A vaccine comprising a PCV nucleic acid that encodes an immunogenic polypeptide of type I or type II PCV strain and a carrier, is useful for treating or preventing congenital tremors in a pig or its progeny (PCV type I is composed of PW-15-PCV and CT-PCV-P7, PCV type II is composed of PW-15-PCV and CT-PCV-P7, PCV type II is composed of PW-15-PCV-P2, -P3, -P4, and CT-PCV-P5, -P6). An isolated PCV strain (II) is useful for diagnosing a pathological cause of congenital tremors in a pig which involves determining whether the pig chas been infected by PCV strain type I or type II. The determination of the infection is effected by detecting the presence of a PCV nucleic acid in a biological sample from the pig, by detecting hybridisation of an oligonucleotide. Optionally, the determination of infection is effected by detecting the presence of PCV polypeptide in a biological sample from the pig. An expression vector (III) encoding a CFC in a biological sample of the pig. An expression vector (III) encoding a CFC in a biological sample of the pig. An expression vector (III) encoding a CFC (II) along with a suitable adjuvant is useful as a whole PCV vaccine, while the antipodies against PCV proteins are used as components of subunit communisation strategies. This sequence represents a porcine circovirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New porcine circovirus (PCV) nucleic acids for use as a component of vaccines for treating or preventing congenital tremors in pigs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-106466/14.
N-PSDB; ABU02908, ABU02913, ABU02917, ABU02924, ABU02931, ABU02941,
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                                                                                      Porcine circovirus genome; PCV; vaccine; type I PCV strain; type II PCV strain; congenital tremor; pig; whole PCV vaccine; passive immunisation; ds.
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Pred. No. 0;
                                                       P1 genome
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                                                       PMWS-Porcine circovirus (PCV)
                                                                                                                                                                                                                                                                                                                                      15-JUN-2000; 2000US-0211710P.
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70.6%;
Best Local Similarity 88.2%;
Matches 1449; Conservative
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                                                                    GIGITACATIGGICTICCAATCACGCTICTCGCATITICCCGCTCACTITCAAAAGTICAGC
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The invention describes an isolated nucleic acid (I) from a porcine circovirus (PCV) where (I) comprises a sequence coding for a circovirus polypeptide. A vaccine comprising a PCV nucleic acid that encodes an immunogenic polypeptide of type I or type II PCV strain and a carrier, is useful for treating or preventing congenital tremore in a pig or its progeny (PCV type I is composed of PR-15-PCV and CT-PCV-P7, PCV type I is composed of PR-15-PCV and CT-PCV-P7, PCV type I is composed of PR-15-PCV and CT-PCV-P5, -P6). An isolated PCV strain (II) is useful for diagnosing a pathological cause New porcine circovirus (PCV) nucleic acids for use as a component of vaccines for treating or preventing congenital tremors in pigs. Porcine circovirus genome; PCV; vaccine; type I PCV strain; type II PCV strain; congenital tremor; pig; whole PCV vaccine; passive immunisation; ds. 5

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of congenital tremors in a pig which involves determining whether the pighas been infected by PCV strain type I or type II. The determination of the infection is effected by detecting the presence of PCV nucleic acid in a biological sample from the pig, by detecting hybridisation of an oligonuclectide. Optionally, the determination of infection is effected by detecting the presence of PCV polypeptide in a biological sample from the pig binding of an antibody that specifically binds a PCV polypeptide. Optionally, the determination of infection is effected by petecting the presence of antibodies directed against a PCV polypeptide in a biological sample of antibodies directed against a PCV polypeptide in a biological sample of the pig. An expression vector (III) encoding a PCV polypeptide is useful as a vector vaccine against congenital tremors. (III) along with a suiteble adjuvant is useful as a whole PCV vaccine, while the antigenic PCV polypeptides are used as components of subunit vaccines. Antibodies against PCV proteins are useful in passive
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                                                                                                                                                                                                                                                                                                                                                            The invention describes an isolated mucleic acid (I) from a porcine circovirus (PCV) where (I) comprises a sequence coding for a circovirus polypeptide. A vaccine comprising a PCV nucleic acid that encodes an immunogenic polypeptide of type I or type II PCV strain and a carrier, is useful for treating or preventing congenital tremors in a pig or its progeny (PCV type I is composed of PK-15-PCV and CT-PCV-P7, PCV type II composed of PK-15-PCV and CT-PCV-P5, -P6).

The congenital tremors in a pig which involves determining whether the pig of congenital tremors in a pig which involves determining whether the pig the infection is effected by detecting the presence of a PCV nucleic acid in a biological sample from the pig, by detecting hybridisation of an oligonucleotide. Optionally, the determination of infection is effected by detecting binding of an antibody that specifically binds a PCV polypeptide. Optionally, the determination of infection is effected by detecting the presence of antibodies directed against a PCV polypeptide in a biological sample of the pig. An antibody that specifically binds a PCV detecting the presence of antibodies directed against a PCV polypeptide in a biological sample of the pig. An aversesion vector (III) encoding a PCV polypeptide is useful as a vector vaccine against congenital tremors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   while the antigenic PCV polypeptides are used as components of subunit vaccines. Antibodies against PCV proteins are useful in passive immunisation strategies. This sequence represents a porcine circovirus
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                                                                                                                                                                                                                                                                                              New porcine circovirus (PCV) nucleic acids for use as a component of vaccines for treating or preventing congenital tremors in pigs.
                                                                                                                                                                                                                                                                  N-PSDB; ABU02909, ABU02916, ABU02923, ABU02930, ABU02949, ABU02956
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Porcine circovirus genome, PCV, vaccine, type I PCV strain, type II PCV strain, congenital tremor, pig, whole PCV vaccine, passive immunisation, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1759 BP; 432 A; 342 C; 510 G; 475 T; 0 U; 0 Other;
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                                                                                                                                                                                                                           Kanitz CL
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                                                                                                                                                                                                                           Choi J,
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                                                                                                                                         15-JUN-2001; 2001WO-US019220.
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Best Local Similarity 84.9%;
Matches 1397; Conservative 0
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                                                                                                                                                                                               (PURD ) PURDUE RES FOUND
                                                         Porcine circovirus
                                                                                 WO200196377-A2
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                                                                                                                                                                                                              The specification describes a polynucleotide that is capable of rolling circle replication (RRD) in an eukaryotic host. The polynucleotide comprises a Rep gene encoding from a virus, sequences that are cis on the polynucleotide such that the Rep protein can bring about RCR of the polynucleotide, an open reading frame encoding a protein of interest capable of being expressed in the host, and optionally a multiple cloning site, where the polynucleotide lacks genes of the virus. The virus is selected from the group of genera of family Geminiviridae, Circoviridae and Nanovirus. The polynucleotide sequence is useful for the discovery of the function of genes in eukaryotic hosts, and for inducing or enhancing a trait in a host eukaryotic cell, for down-regulating a gene in a plant
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                                                                                                                                                                                  GCTCCATTTAAATACCCACACCAATGTCGAGCACACAGGCCTCGGCTATGCGCTCCAAAA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotide capable of rolling circle replication in host, useful for discovery of gene function, comprises Rep gene, sequences that are cis on the polynucleotide and open reading frame encoding protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rolling circle replication; RCR; Rep gene; gene function; Geminivirus;
Circovirus; Nanovirus; gene therapy; PCV; ds.
                                                                                                                                                       TAATCTTAAAGACCCCCCCCTTAAACCCTTAAATGAATAAAAATAAAAATTACGATTACGATGT
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                                           GATGAGGCTACAAACCTCTAGAAATGTGGACCACGTAGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     of a plasmid pCI-PCV1-Luc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleotide sequence
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or in mammalian cell and thus altering or even eliminating the function of that gene, as gene sequence delivery tools for mammalian genomic approaches, for gene therapy applications (for delivering therapeutic or complementing gene products to organisms or cells), and in whole animal genomics. The present sequence represents a plasmid pCI-PCVI-Luc, comprising the PCR Rep gene and the luciferase reporter gene
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                                                                                                   Sequence 7460 BP; 1910 A; 1677 C; 1886 G; 1987 T; 0 U; 0 Other;
                                                                                                                              Query Match 67.5
Best Local Similarity 86.8
Matches 1357; Conservative
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                                                                                                                                                                                                     ATAAGAAAGGTTAAAGTTGAATTCTGGCCCTGCTCCCCCATCACCCCAGGGTGATAGGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rep gene; rolling circle replication;
GTGCTGCCGCTGCCGAAGTGCGCTGGTAATACTACAGCAGCGCACTTCTTTCACTTTTAT
           GTGCTGCCGCTGCCGAAGTGCGCTGGTAATACTACAGCAGCGCACTTCTTTCACTTTTAT
                                AGGATGACGTATCCAAGGAGGCGTTACCGCAGAAGAAGACACCGCCCCCCGCAGCCATCTT
                                                 AGGATGACGTGGCCAAGGAGGCGTTACCGCAGAAGAAAGGACCCGCCCCCCGCAGCCATCTT
                                                                 GGCCAGATCCTCCGCCGCCCCCTGGCTCGTCCACCC-----CCGCCACCGCTACCGT
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The invention relates to a polymucleotide capable of eliciting an immunisation reaction in a eukaryotic host to a peptide or polypeptide. The polymucleotide encodes the peptide or polypeptide, and contains elements of a viral genome (i.e. the Rep gene) that is capable of rolling circle replication. The peptide or polypeptide is capable of expression in the eukaryotic host. Also included are constructing a polymucleotide capable of eliciting an immunisation reaction in a host (comprising final comprision) and immunisation reaction comprises elements of a viral genome that is capable of rolling circle replication and immunishing a host comprising administering a composition comprising the polymucleotide into the host. Substantially higher levels of ggd antibody induction were seen in mice injected with immunogenic protein insert linked to a rolling circle replican mammalian expression vector. Levels of IgG antibody through successive bleeds were higher for both luciferase and beta-galactosidase expression cassettes linked to a porcine Circovirus cassette, as compared to non-rolling circle replicon in a eukaryotic host is useful in vaccine or gene therapy applications, or for eliciting an immunisation reaction in a eukaryotic cell or beta-galactosidase. The polymucleotide capable of rolling circle replicons or popplications, or for eliciting an immunisation reaction in a eukaryotic cell or substruction of genes in eukaryotic cell, or for downregulations, or for eliciting an immunisation reaction in a eukaryotic cell or enhancing a function or trait in a host eukaryotic cell, or for downregulating agene in a plant or mammalian cells, which alters or even cellaniating an immunisation reaction in the host elicited by the peptide or polymeteride of the genes the eukaryotic cell or polymeteride of the subservance (termed polymeteride of the present sequence of polymeteride of the presen
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                                                                                                                                                                New rolling circle DNA replicons or polynucleotides, useful in vaccine gene therapy applications, for eliciting an immunization reaction in a eukaryotic host, or for inducing or enhancing a function or trait in a
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Pred. No. 0;
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    Mccormick
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86.8%;
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          ACAGTCACCAAAGACCCCGTCTCCAAAAGGGTACTCACAGCAGTAGACAGGTCGCTGCGC 1026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rolling circle replication; RCR; Rep gene; gene function; Geminivirus;
Circovirus; Nanovirus; gene therapy; PCV; ss.
                              TATGACCCCTATATTAACTACTCCTCCGCCACACCATAAGGCAGCCCTTTACCTACAC
                                                                                                                                                                                            Nucleotide sequence of a construct comprising the PCV Rep gene.
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Porcine circovirus.
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Example 1; Fig 5; 61pp; English.

The specification describes a polynucleotide that is capable of rolling circle replication (RCR) in an eukaryotic host. The polynucleotide comprises a Rep gene encoding from a virus, sequences that are cis on the polynucleotide such that the Rep protein can bring about RCR of the polynucleotide, an open reading frame encoding a protein of interest capable of being expressed in the host, and optionally a multiple cloning site, where the polynucleotide lacks genes of the virus. The virus is selected from the group of genera of family Geminiviridae, Circoviridae and Nanovirus. The polynucleotide sequence is useful for the discovery of the function of genes in eukaryotic hosts, and for inducing or enhancing a trait in a host eukaryotic cell, for down-regulating a gene in a plant of that gene, as gene sequence delivery tools for mammalian genomic of that gene, as gene sequence delivery tools for mammalian genomic approaches, for gene therapy applications (for delivering therapeutic or complementing gene products to organisms or cells), and in whole animal complementing gene products to organisms or cells), and in whole animal complementing construct comprising the continual control of its own promoter, and has the putative coat transcriptional control of its own promoter, and has the putative coat protein inactivated by insertion of the bacterial cloning vector

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Construct 1; PCV; ds.
                                              780 CGAAAGACGGGTATCTTCAATTCCCGCCTTTCTACAGAATTTGTACTCACATAAAAGGA
                                                                                                                                                                  G---GATACTCGCAGCCATCTTGGAATGTTAACTACCTCAAATTCAACATCGGCCAGTTC
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(MCCO/) MCCORMICK A.
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               BP; 1216 A; 1277 C; 1514 G; 1278 T; 0 U; 0 Other;
                                           Length 5285;
                                        Query Match 67.4%; Score 1195.8; DB 4; Length Best Local Similarity 87.7%; Pred. No. 0; Matches 1331; Conservative 0; Mismatches 177; Indels
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gene therapy applications, for eliciting an immunization reaction in a eukaryotic host, or for inducing or enhancing a function or trait in a host eukaryotic cell.

Example 1; Fig 5; 51pp; English

The invention relates to a polynucleotide capable of eliciting an immunisation reaction in a eukaryotic host to a peptide or polypeptide. Immunisation reaction in a eukaryotic host to a peptide or polypeptide. In the polynucleotide encodes the peptide or polypeptide, and contains of correct replication. The peptide or polypeptide is capable of rolling circle replication. The peptide or polypeptide is capable of expression in the eukaryotic host. Also included are constructing a polynucleotide inserting a sequence encoding a peptide or polypeptide into the inserting a sequence encoding a peptide or polypeptide into the polynucleotide where the polynucleotide comprises elements of a viral genome that is capable of rolling circle replication and immunishing a host comprising daministering a composition comprising the polynucleotide on the host. Substantially higher levels of IgG antibody induction were seen in mice injected with immunogenic protein insert linked to a rolling circle replication mammalian expression vector. Levels of IgG antibody through successive bleeds were higher for both luciferase and non-rolling circle replication mammalian expression vector. Levels of Indea and into a cassette, as compared to non-rolling circle replication linked vectors or injection with saline alone, vector without insert, purified luciferase or beta-galactosidase. The polynucleotide capable of rolling circle replication in a eukaryotic host is useful in vaccine or gene therapy application in a eukaryotic or the discovery of the function of genes in eukaryotic cell, or for downered a function of that gene. The anoillary protein is useful for replication a function of that gene. The anoillary protein is useful for replication a immunisation in the host elicited by the peptide or polypeptide. The present sequence (termed Construct 1) is a control of the inventor control of its own prometer and the coat control of its own prometer and the coat protein gene is inactivated by insertion of the vector

Sequence 5285 BP; 1216 A; 1276 C; 1515 G; 1278 T; 0 U; 0 Other;

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1621 1561 TAGAGAGCTTCTACAGCTGGGACAGCAGTAGAGAGTACCATTCCTGGGGGGCCTGATTG 1741 CAGTAGGTGTCCCTAGGCTCAGCAAAATTACGGGCCCACTGGCTCTTCCCACAACCGGGC 1501 AATGGATACCGGTCACACACTCTCAGTAGATCATCCCAAGGTAACCAGCCATAAAATCA 240 300 360 CTGGTAATCAAAATACTGCGGGCCAAAAAGGAACAGTACCCCCTTTAGTCTCTACAGTC TAGAGAGCTTCTACAGCTGGGACAGCAGTTGAGGAGTACCATTCCTGGGGGCCCTGATTG CTGGTAATCAAAATACTGCGGGCCAAAAAAGGAACAGTACCCCCTTTAGTCTCTACAGTC TCCAAAACAACATCTTCTCCCATGATATCCATCCCACCACTTATTTCTACTAGGCTTC TCCAAAACAACAACTTCTTCTCCATGATATCCATCCCACCACTTATTTCTACTAGGCTTC CAGTAGGTGTCCCTAGGCTCAGCAAAATTACGGGCCCCACTGGCTCTTCCCCACAACCGGGC GGGCCCACTATGACGTGTACAGCTGTCTTCCAATCACGCTGCTGCTTTCCCGCTCACT GGTACCTCCGTGGATTGTTCTCCAGCAGTCTTCCAAAATTGCAAAGTAGTAATCCTCCGA Gaps 6 Length 5285; Score 1195.8; DB 8; Length Pred. No. 0; 0; Mismatches 177; Indels 67.4%; Query Match
Best Local Similarity 87.7
Matches 1331, Conservative 1860 1800 181 1560 1740 1680 1620 61 121 241 301 361

λ̈́	421	TTCAAAAGTTCAGCCGCGGGAAATTTCTCACATACGTTACAGGAAACTGCTCGGCT 480
qq	1440	13
δ	481	ACAGTCACCAAAGACCCGGTCTCCAAAAGGGTACTCACAGGAGTAGACAGGTGCTGCC 540
Dβ	1380	ACAGTCACCAAAGACCCCGTCTCCAAAAGGGTACTCACAGCAGTAGACAGGTCGCTGCGC 1321
ර් ර	4 (TTCCCCTGGTTCCGCGGAGCTCCACATCGATAAGTATGTGGCCTTCTTACTGCAGTAT 600
an ,	v	1
ð i	0 1	TCTTTATTCTGCTGGTCGGTTCCTTTCGCTTTCTCGATGTGCCGCGCGCG
a 8	1260	ITTATTATUGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
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ò	721	GTTCTACCCTCTTCCAAACCTTCCTGGCCACAAAAAAAAA
qq	1140	TIACCCTCTTCCAAACCTTCCTCCGCAAACAAAAAAAAAA
č	781	AGCICCCGTATTTTGTTTTTTCTCCTCGGAAGGATTATTAAGGGTGAACACCCACTC 840
qq	1080	AGCTCCCGTATTTTGTTTTTCTCCTCCGGAAGGATTATTAAGGGTGAACACCCACC
ογ	841	0
qq	1020	96
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δλ	961	ACGIAICCAAGGAGGCGITACCGCAGAAGAAGACACGCCCCCGCAGCCAICTIGGCCAG 1020
q ₀	900	acgregecaaggaggegtracegaagaagaaggaccegececegeagcaterregaaae 841
ŏ	1021	ATCTCCGCGCGCCCCTGGCTCGTCCACCCCGCCACCGCTACCGTTGGAGA 1074
QQ	840	Arctrocesasasasacararriescacacececerroasaacestracasareses 781
ò	1075	7
qq	780	cgaaagacgggrandtricaatroccgcctrictacagaattrgtactcaccataaaagga 721
Š	1135	ACCACAGTCAGAACGCCCTCCTGGGGGGGGGCATGATGAGATTTAATATTGACGACTTT 1194
qq	720	ggaracrogcadccarcridgaargiraacracrocaaarircaacarcacrarro 664
ò	1195	0
qq	663	ciccicicercadacadeaceaececracecracerrecaaracracerarrada 604
ò	1255	AAGSTTAAGSTTGAATTCTGGCCCTGCTCCCCATCACCAGGGTGATAGGGGGGAGTGGC 1314
Q	603	54
ò	1315	TCCACTGCTGTTATTCTACATGATAACTTTGTAACAAAGGCCACAGCCCTAACCTATGAC 1374
qq	543	aciditatrateriogatgecaaciticiaaceeereeaceacitigged 48
ò	1375	CGT 1
ДQ	483	ccciaiaitaaciaciccicciacacacacaraagaaagacarriaacciaccacracagg 424
ò		
Ωp	423	TACTTCACCCCAAACCTGGACCAAACAATTGATTGGTTCCACCCAATAATAA 364

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circle replication (RCR) in an eukaryotic host. The polymucleotide comprises a Rep gene encoding from a virus, sequences that are cis on the polymucleotide such that the Rep protein can bring about RCR of the polymucleotide, an open reading frame encoding a protein of interest capable of being expressed in the host, and optionally a multiple cloning site, where the polymucleotide lacks genes of the virus. The virus is selected from the group of genera of family Geminiviridae, Circoviridae and Nanovirus. The polymucleotide sequence is useful for the discovery of the function of genes in eukaryotic hosts, and for inducing or enhancing a trait in a host eukaryotic cell, for down-regulating a gene in a plant or in mammalian cell and thus altering or even eliminating the function of that gene, as gene sequence delivery tools for mammalian genomic approaches, for gene therapy applications (for delivering therapeutic or complementing gene products to organisms or cells), and in whole animal genomics. The present sequence represents a construct in which the SW40 promoter and origin of replication was deleted. This context contains the proverse or capable or the transcriptional control of its own promoter. The contains the proventer with the PVV origin of replication, in the context of a vector that contains the present sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polynucleotide capable of rolling circle replication in host, useful discovery of gene function, comprises Rep gene, sequences that are on the polynucleotide and open reading frame encoding protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        specification describes a polynucleotide that is capable of rolling
                                                                                                                                                                                                                                                                                       gene, gene function, Geminivirus, PCV, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contains a selectable and screenable marker gene (GFP-zeocin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5650 BP; 1372 A; 1333 C; 1516 G; 1429 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                     Nucleotide sequence of a construct comprising the PCV Rep gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1195.8; DB 4; Length
Pred. No. 0;
0; Mismatches 177; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              resistance), but which cannot replicate in COS-7 cells
                                                                                                                                                                                                                                                                                             RCR; Rep c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (LARG-) LARGE SCALE BIOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Fig 6; 61pp; English.
AGGAATCAGCTTTGGAT 1511
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87.7%;
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                                                                                                                                                                                                                                                                                               replication;
                                                                                                                                                                                                                                                                                                             Circovirus; Nanovirus; gene
                    AGAAACCAGCTGTGGCT
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Best Local Similarity 87.7
Matches 1331; Conservative
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Porcine circovirus.
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1495
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1434 1254 1314 1194 1193 ACAGTCACCAAAGACCCCGTCTCCAAAAGGGTACTCACAGCAGTAGACAGGTCGCTGCGC 1134 ACGTATCCAAGGAGGCGTTACCGCAGAAGACACCGCCCCCCCGCAGCCATCTTGGCCAG 1020 1074 TAGAGAGCTTCTACAGCTGGGACAGCAGTTGAGGAGTACCATTCCTGGGGGGCCTGATTG 1554 133 TTCCCCTGGTTCCGCGGAGCTCCACACTCGATAAGTATGTGGCCTTCTTTACTGCAGTAT 1074 TCTTTATTCTGCTGGTCGGTTCCTTTCGCTTTCTCGATGTGGCAGCGGGCACCAAAATAC 1014 240 300 360 900 AGGAAAAATGGCATCTTCAACACCCGCCTCTCCCGCACCTTCGGATATACTGTCAAGGCT 1134 420 480 540 900 99 960 654 720 954 780 894 840 834 774 ccecrecceaagrececregraaracracaecececrerrrrrcacrrrraraegare 714 593 CGAAAGACGGGTATCTTCAATTCCCGCCTTTCTACAGAATTTGTACTCACCATAAAAGA 534 CTGGTAATCAAAATACTGCGGGCCAAAAAGGAACAGTACCCCCTTTAGTCTTACAGTC TCCAAAACAACAACTTCTTCTCCATGATATCCATCCCACCACTATTTCTACTAGGCTTC 1373 CAGTAGGTGTCCCTAGGCTCAGCAAAATTACGGGCCCACTGGCTCTTCCCACAAACGGGC 1313 GGCCCACTATGACGTGTACAGCTGTCTTCCAATCACGCTGCTGCATCTTCCCGCTCAT TTCAAAAGTTCAGCCAGCCGCGGAAATTTCTCACATACGTTACAGGAACTGCTCGGCT GTTCTACCCTCTTCCAAACCTTCCTCTCCGCAAACAAATAATCAAAAAGGGAGATTGGA TATGGGGTGGGGCGCTTTTCTTGCTTGCATTTTCACTGACGCTGCCGAGGTGCTG 713 ACGTGGCCAAGGAGGCGTTACCGCAGAAGAAGGACCCGCCCCCCGCAGCCATCTTGGAAAC ATCCTCCGCCGCCCCTGGCTCGTCCACCC-----CCGCCACCGCTACCGTTGGAGA AATGGATACCGGTCACACAGTCTCAGTAGATCATCCCAAGGTAACCAGCCATAAAAATCA TCCAAAACAACATCTTCTTCCATGATATCCATCCACCACTTATTTCTACTAGGCTTC CAGTAGGTGTCCCTAGGCTCAGCAAAATTACGGGCCCACTGGCTCTTCCCACAACCGGGC CACTICACCTIGITAAAAGICTGCTICTTAGCAAAATICGCAAACCCCTGGAGGTGAGGA CACTICACCITIGITIAAAAGICIGCITICITIAGCAAAATICGCAAACCCCTGGAGGTGAGGA GTTCTACCCTCTTCCAAACCTTCCTCGCCACAAACAAAATAATCAAAAAGGGAGATTGGA AGCTCCCGTATTTTGTTTTTCTCCTCCGGAAGGATTATTAAGGGTGAACACCCTC TTATGGGGTTGCGGCCCCTTTTCTTGCTTGGCATTTTCACTGACGCTGCCGAGGTGCTG CCGCTGCCGAAGTGCGCTGGTAATACTACAGCAGCGCACTTCTTTCACTTTTATAGGATG CTGGTAATCAAAATACTGCGGGCCAAAAAGGAACAGTACCCCCTTTAGTCTCTACAGTC GGGCCCACTATGACGTGTACAGCTGTCTTCCAATCACGCTGCTGCATCTTCCCGCTCACT TTCAAAAGTTCAGCCAGCCGGGAAATTTCTCACATACGTTACAGGAAACTGCTCGGCT ACAGTCACCAAAGACCCCGTCTCCAAAAGGGTACTCACAGGCAGTAGACAGGTCGCTGCGC TTCCCCTGGTTCCGCGGAGCTCCACTCGATAAGTATGTGGCCTTCTTTACTGCAGTAT 1CTTTATTCTGCTGGTTGGTTTCCTTTTCTCTGATGTGGCAGCGGGCACCAAATAC 1613 1553 1493 361 1253 1073 1013 1433 1021 1075 181 241 301 481 781 961 61 121 421 541 841 653 601 661 721 953 893 833 901 773 ద 셤 셤 셤 셤 셤 셤 g 셤 g ò Š ò ઠે 셤 ઠે ð ò ò ઠે δ ò 셤 ઠે a ð 셤 ò a ò g ð 셤 a

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1135 ACCACAGTCAGAACGCCTCCTGGGCGGTGGACATGATGATTAATATTGACGACTTT 1194	1195 GITCCCCGGGGGGGGCCAACAAATCTCTATACCCTTTGAATACTACAGAATAAGA 1254	1255 AAGGTTAAGGTTGAATTCTGGCCCTGCTCCCCATCACCCAGGGTGATAGGGAGTGGGC 1314	1315 TCCACTGCTGTTATTCTAGATGATAACTTTGTAACAAAGGCCCACAGCCCTAACCTATGAC 1374	1375 CCATATGTAAACTACTCCTCCGCCATACAATCCCCCAACCCTTCTCCTACCACTCCGT 1434	1435 TACTTCACACCCAAACCTGTTCTTGACTCCACCATTGATTACTTCCAACCAA	1495 AGGAATCAGCTTTGGAT 1511
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Search completed: August 5, 2005, 02:42:15 Job time: 987 sec8

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AY099498 Porcine AX379562 Sequence

AX379560 Sequence AY099496 Porcine AX379564 Sequence

AX379561 Sequence AX379563 Sequence

AY099495 Porcine c AY099499 Porcine c Y09921 Porcine cir

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AF305532 Porcine C AF305533 Porcine C AX379559 Sequence AX379565 Sequence AX379565 Sequence AX226280 Sequence AX226280 Sequence AX226281 Sequence AX226281 Sequence AX26281 Sequence AX26281 Sequence AX26281 Sequence AX26281 Sequence AX26281 Sequence AX26281 Sequence AX264817 Sequence

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Minimum Maximum Database

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/db_xref="GI:9392645"
/translation="MTYPRRRYRRHRPRSHLGQILRRRPWLVHPRHRYRWRRKNGI
FNTRLSRTFGYTVKATTVRTPSWAVDMMRFNIDDFVPPGGGTNKISIPPEYYRIRKVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Porcine circovirus 2
Viruses; seDNA viruses; Circoviridae; Circovirus.

1 (Dases 1 to 1768)

Penaux,M., Halbur,P.G., Gill,M., Toth,T.B. and Meng,X.J.

Genetic characterization of type 2 porcine circovirus (PCV-2) from pigs with postweaning multisystemic wasting syndrome in different geographic regions of North America and development of a differential PCR-restriction fragment length polymorphism assay to detect and differentiate between infections with PCV-1 and PCV-2 20341537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fenaux, M., Halbur, P.G., Gill, M., Toth, T.E. and Meng, X.J. Direct Submission
Submitted (08-WAY20000) VWRCVM, Virginia Tech, 1410 Pric. Road, Blacksburg, VA 24061, USA
Location/Qualifiers
1. 1768
/organism="Porcine circovirus 2"
/mol type="genomic DNA"
/isolate="40895"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nrzowysz 1768 bp DNA linear VRL
Porcine circovirus type 2 isolate 40895 complete genome.
AF264042
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'protein_id="AAF87235.1"
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                                                      AX379560
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complement(37...738)
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                                                                                                                        /protein_id="AAF87236.1"
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VERWPCSPITOGDRGYGSTAVILDDNFVPKATALTYDPYVNYSSRHTIPOPFSYHSRY
FTPKPVLDSTIDYFQPNNKRNQLWIRLQTSRNVDHVGLGTAFENSKYDQDYNIRVTMY
VQFREFNLKDPPLNP"
                                                                                                                                                                                                                                                                       VGEEGNEEGRTPHLQGFANFVKKQTFNKVKWYLGARCHIEKAKGTDQONKEYCSKEGN
LieCGAPREGOGRBDLSTAVSTLLESSGSLVTWARADHYDHYDRARFAELLKVSGRM
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GWLPWDDLLRLCDRYPLIVETKGGTVPFLARSILITSNQTPLEWYSSTAVPAVEALYR
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/db xref="GI:9392637"
/translation="MPSKKNGRSGPQPHKRWVFTLANPSEDERKKIRELPISLFDYFI
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translation="MTYPRRRYRRRRHRPRSHLGQILRRRPWLLHPRHRYRWRRKNG"
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Pred. No. 0;
0; Mismatches 156; I
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/product="replicase"
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/gene="rep"
822. .1766
/gene="rep"
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Viruses, SaDNA viruses, Circoviridae, Circovirus.

Viruses, SaDNA viruses, Circoviridae, Circovirus.

Viruses, Lto 1768)

Fenaux,M., Halbur,P.G., Gill,M., Toth,T.E. and Meng,X.J.
Genetic characterization of type 2 porcine circovirus (PCV-2) from pigs with postweaning millisystemic wasting syndrome in different differential PCR-restriction fragment length polymorphism assay to detect and differentiate between infections with PCV-1 and PCV-2 20341537
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2 (bases 1 to 1768)
Penaux, M., Halbur, P.G., Gill, M., Toth, T.E. and Meng, X.J.
Direct Submission
Submitted (08-MAY-2000) VMRCVM, Virginia Tech, 1410 Prices Fork
                                                                                                                                                                                                                                                                                               206 ACADADAGGAATCAGCTTTGGCTGAGGCTACDAAACCTCTAGAAATGTGGACCACGTAGGCC
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                                                          TGGGCTCCACTGCTGTTATTCTAGATGATAACTTTGTAACAAAGGCCACAGCCCTAACCT
                                                                                TGGGCTCCACTGCTGTTATTCTAGATGATAACTTTGTAACAAAGGCCACAGGCCCCTAACCT
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/produc="putative capsid protein"
/protein_id="AAR87229.1"
/db_xref="GI:9392636"
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mol type="genomic DNA"
isolate="26607"
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/gene="cap"
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Location/Qualifiers
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           TCTACCCTCTTCCAAACCTTCCTCGCCACAAACAAATAATCAAAAAGGGAGATTGGAAG
                       CTCCCGTATTTTCTTGCGCTCGTCTTCGGAAGGATTATTCAGCGTGAACACCCCTTTT
                                                                                                              CCGAGGTGCTGCCGCTGCCGAAGTGCGCTGGTAATACT--TACAGCGCACTTCTTTCGTT
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Anyang 6-Dong, Anyang, Gyeonggi
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Porcine circovirus type 2 isolate JHP, complete genome
                                                                                                                                                                                                                                                                                                                                                             and Choi, E.J.
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                                                                                                                                                                                                                                                           Viruses, seDNA viruses, Circoviridae, Circovirus.

1 (bases 1 to 1768)
Park, J.H., Roh, I.S., Song, J.Y., Cha,S.H. and Choi Direct (borsesion Submitted (07-JUN-2002) Virology Division, Nation Research and Quarantine Service, Anyang 6-Dong, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /isolation source="pig with ponephropathy syndrome (PDNS)" /db.xref="texon:85708" /country="South Korea" complement (37. 738) /codon_start=1
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89.8%; Pred. No. 0;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                            Porcine circovirus
Porcine circovirus
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Matches 1533; Conservative
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Porcine circovirus type 2 strain KSY-2 from Korea, complete genome.
AF544024
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                                                                                                                                                                                                 ATGTACAATTCAGAGAATTTAATCTTAAAGACCCCCCCCTTAAACCCCTAAATGAATAAAA 1669
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206 ACAAAAGGAATCAGCTTTGGCTGAGGCTACAAAACTCTGAGAAATGTGGACCACGTAGGCC
                                                                                                                            TCGGCACTGCGTTCGAAAACAGTATATACGACCAGGACTACAATATCCGTGTAACATGT
                                                                                                                                                 146 TCGGCACTGCGTTCGAAAACAGTAAATACGACCAGGACTACAATATCCGTGTAACCATGT
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Direct Submission
Submitted (08-SEP-2002) College of Veterinary Medicine, Chungk National University, #48, Gaeshin-dong, Heungduk-ku, Cheongju 361-763, Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 isolated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssDNA viruses; Circoviridae; Circovirus.

1 (bases 1 to 1768)

Kim,K.M., Song,Y.K., Park,H.S. and Kang,S.Y.

Characterization of porcine circovirus type 2 isc
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                                                                                                                                                                                                                                                                                                            N
                                                                                                                                                                                                                                                                                              complement (37, .738)
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Porcine circovirus 2
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DEFINITION
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Porcine circovirus 2
Porcine circovirus 2
Viruses; ssDNA viruses; Circoviridae; Circovirus.

1 (bases 1 to 1768)
Fenaux, M., Halbur, P.G., Gill, M., Toth, T.E. and Meng, X.J.
Genetic characterization of type 2 porcine circovirus (PCV-2) from pigs with postweaning multisystemic wasting syndrome in different geographic regions of North America and development of a differential PCR-restriction fragment length polymorphism assay to different and differentiate between infections with PCV-1 and PCV-2.
                                           AGGCTACCACAGTCAGAACGCCCTCCTGGGCGGTGGACATGAGATTTAATATTGACG
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Fenaux, M., Halbur, P.G., Gill, M., Toth, T.E. and Meng, X.J.
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|db_xref="G1:992642"
|translation="MTYPRRRYRRRHRPRSHLGQILRRRPWLVHPRHRYRWRKNGI"
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FTPRPVLDSTIDYFQDNNKRNQLWLRLQTSRNVDHVGLGTAFBNSKYDQDYNIRVTWY
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VGEEGNEEGRIPHLQGFANFVKKQTFNKVKWYLGARCHIEKAKGTDQQNKEYCSKEGN
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RITSLVFWKNATEQSTEEGGGFVTLSPPCPFYEINY"
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                                                                       /organism="Porcine circovirus
/mol_type="genomic DNA"
/isolate="40856"
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/protein_id="AAF87234.1"
/db_xref="GI:9392643"
    Direct Submission
Submitted (08-MX-2000) VMRCVM,
Road, Blacksburg, VA 24061, USA
Location/Qualifiers
                                                                                                                 /db_xref="taxon:85708"
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S Penaux, M., Halbur, P.G., Gill, M., Toth, T.E. and Meng, X.J.

Direct Submitsation

L Submitted (108-MAY-2000) VMRCVM, Virginia Tech, 1410 Prices Fork
Road, Blacksburg, VA 24061, USA

Location/Qualifiers

I. .1768

/ organism="Porcine circovirus 2"

// mol type="genomic DNA"

// isoTate="26606"

/ db xref="taxon:85708"

/ country="USA: Iowa"

complement (37. .738)

/ complement (37. .738)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="myterrrerrerrerrer"/
FNTRLSRTFGYTVKRTTVTTPSWAVDWMRFKLDDFVPPGGGTINKISIPFEYRIRKVK
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PTPKPVLLOSTIDYFQDRGVGSTAVTLDDNFVPKAKALTYDPYVNYSSRHTIRQDFSYHSRY
VQFREFNLKDPPLNP"
                            1609
                                                                                                                                                                                                                                                                                                                     Viruses, Sebna viruses, Circoviridae, Circovirus.

1 (bases 1 to 1768)
Fenaux,M., Halbur,P.G., Gill,M., Toth,T.E. and Meng,X.J.
Genetic characterization of type 2 porcine circovirus (FCV-2) from pigs with postweaning multisystemic wasting syndrome in different geographic regions of North America and development of a differential PCR-restriction fragment length polymorphism assay to detect and differentiate between infections with PCV-1 and PCV-2 2011.
                                                                                 ATGTACAATTCAGAGAATTTAATCTTAAAGACCCCCCACTTAAACCCTAAATGAATAAAA 1669
                                                                                                                                                                                                                                     VRL 23-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tränslation="mpskkngrsgpqphkkwyftlnnpsederkkirelpislfdyfi
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                                                     87
                                                                                                            30
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                                                                                               TCGCCACTGCGTTCGAAAACAGTATATACGACCAGGACTACAATATCCGTGTAACCATGT
                                                                                                                                                                                                                                    linear VRL complete genome
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2 isolate 26606
                                                                                                                                     ATAAAAACATTACGATGTGATAACAAA 1697
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                                                                                                                                                                                                                                 AP264038
Porcine circovirus type
AP264038
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Viruses:
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822. .1766
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VERSION
KEYWORDS
SOURCE
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MEDLINE
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GWLPWDDLLRLCDRYPLTVETKGGTVPPLARSILITSNQTPLEWYSSTAVPAVEALYR
RITSLVFWKNATEGSTEEGGQFVTLSPPCPEFPYEINY"
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                                                                                                                                                                                                                              TACCTCCGTGGATTGTTCTCCAGCAGTCTTCCAAAATTGCAAAGTAGTAATCCTCCGATA
                                                                                                                                                                                                                                                                                                                               GAGAGCTTCTACAGCTGGGACAGCAGTTGAGGAGTACCATTCCTGGGGGCCTGATTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 CAAAACAACAACTICTTCTCCCATGATATCCATCCCACCACTTATTTCTACTAGGCTTCCA
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                                                                                                                           DB 14; Length 1768
                                                                                                                                                                            19;
                                                                                                                                                                            158; Indels
                                                                                                                           Score 1367.2;
Pred. No. 0;
                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
2 (bases 1 to 1768)
Fenaux, M., Halbur, P.G., Gill, M., Toth, T.E. and Meng, X.J.
Direct Submission
Submitted (08-MX-22000) VMRCVM, Virginia Tech, 1410 Pric
Road, Blacksburg, VA 24061, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 14; Length 1768;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1364; DB 14;
Pred. No. 0;
); Mismatches 160;
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                                                                                                                 /organism="Porcine circovirus
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complement(37. .738)
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89.5%;
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Best Local Similarity 89.5
Matches 1529; Conservative
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/mol type="genomic DNA"
/isolate="SPA2"
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Pred. No. 0;
0; Mismatches
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                                                                         /db_xref="taxon:85708"
/country="Spain"
complement(37. .738)
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larity 89.3%;
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 Score 1346.4; DB 14; Lengt
Pred. No. 0;
0; Mismatches 171; Indels
 75.9%;
88.9%;
Query Match 75.9
Best Local Similarity 88.9
Matches 1518; Conservative
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/product="putative capsid protein"
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/product="putative"
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                                                                      ATGTACAATTCAGAGAATTTAATCTTAAAGACCCCCCACTTAAAACCCTAAATA 30
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Mankertz, A., Domingo, M., Folch, J.M., LeCann, P., Jestin, A.,
Segates, J., Chmislewicz, B., Plana-Duran, J. and Soike, D.
Direct Submission
Submitted (03-NOV-1999) P24, Robert Koch Institut, Nordufer 20,
Forcine circovirus 2
Porcine circovirus 2
Viruses; seDNA viruses; Circovirus.
Viruses; seDNA viruses; Circoviridae; Circovirus.
Viruses; asDNA viruses; Circoviridae; Circovirus.
Viruses; Domingo,M., Folch,J.M., LeCann,P., Jestin,A., Segales,J., Chmielewicz,B., Plana-Duran,J. and Soike,D. Virus Res. 66 (1), 65-77 (2000)
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GER1,
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2 isolate (
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FNTRLSRTFGYTVKATTVRTPSWAVDWMRFNIDDFVPPGGGTNKISIPFEYYRIRKVK
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88.9%; Pred. No. 0;
ive 0; Mismatches 171; Indels
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Porcine circovirus 2
Viruses; seDNA viruses; Circoviridae; Circovirus.

1 (bases 1 to 1768)
Mankertz, A., Domingo, M., Folch, J. M., LeCann, P., Jestin, A., Segales, J., Chmielewicz, B., Plana-Duran, J. and Soike, D.
Characterisation of FVC2 isolates from Spain, Germany and France
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Submitted (03-NOV-1999) P24, Robert Koch Institut, Nordufer:
Berlin 13353, Germany
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GWLPWDDLLALCDRYPLTVGTKGGTVPFLARSILITSNQTPLEWYSSTAVPAVEALYR
RITSLVFWKNATEQSTEEGGGFVTLSPPCPEFPYEINY"
                                         1610 AICTACAATICAGAGAATITAATCITAAAGACCCCCCACTIAAACCCTAAAIGAATAAAA 1669
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Mankertz,A., Domingo,M., Folch,J.M., LeCann,P., Jestin,A.,
Mankertz,A., Chmielewicz,B., Plana-Duran,J. and Soike,D.
Direct Submission
Submitted (03-NOV-1999) P24, Robert Koch Institut, Nordufer 20,
Berlin 13353, Germany
Location/Qualifiers
146 TCGGCACTGCCTTCGAAAACAGTAAATACGACCAGGACTACAATATCCGTGTAACCATGT
                                                                                 86 ATGTACAATTCAGAGAATTTAATCTTAAAGACCCCCCACTTAAACCCTAAAT---TAATA
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/protein_id="AAF35295.1"
/db_xref="G1:7021348"
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/mol_type="genomic DNA"
/isolate="GER2"
/db_xref="taxon:85708"
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/protein_id="AAF35294.1"
/db_xref="G1:7021347"
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Porcine circovirus type 2 isolate SPA3, complete genome.
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Porcine circovirus 2
Porcine circovirus 2
Viruses; BBNA viruses; Circoviridae; Circovirus.
1 (Dases 1 to 1768)
Mankertz,A., Domingo,M., Folch,J.M., LeCann,P., Jestin,A., Segales,J., Chmielewicz,B., Plana-Duran,J. and Soike,D.
Characterisation of PCV-2 isolates from Spain, Germany and France Virus Res. 66 (1), 65-77 (2000)
                                                                             1130 AGGCTACCACAGTCAGAACGCCCTCCTGGGCGGTGGACATGATGAAGATTTAATATTGACG
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Mankertz,A., Domingo,M., Folch,J.M., LeCann,P., Jestin,A.,
Segales,J., Chmielewicz,B., Plana-Duran,J. and Soike,D.
Direct Submission
Submitted (03-NOV-1999) P24, Robert Koch Institut, Nordufer
Berlin 13353, Germany
Location/Qualifiers
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0; Mismatches 173;
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Best Local Similarity 88.8
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PNTRLSRTFGYTVKATTVTTPSWAVDWMRFNINDFVPPGGGTNKISIPPEYYRIRKVK
PREWPCSPITGGBRGVGSTAVILDDNFVTKATALTYDPYVNYSSRHTIPQPFSYHSRY
PTPRPVLDRTIDYPQPNNKKNQLWLRLGTSANVDHVGLGTAFENSKYDQDYNIRVTMY
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LAMECGAPREGOGRSDLSTAVSTLLESGSLVTVARQHPVRNFRGTAELLKVSGKM
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           ATGTACAATTCAGAGAATTTAATCTTAAAGACCCCCCACTTAAACCCTAAATGAATAAAA 1669
                                                                                                                                           circular VRL 23-FEB-2000 complete genome.
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                       86 ATGTACAATTCAGAGAATTTAATCTTAAAGACCCCCCACTTAAACCCTAAAT---TAATA
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Mankertz, A., Domingo, M., Folch, J.M., LeCann, P., Jestin, A., Segales, J., Chmielewicz, B., Plana-Duran, J. and Solke, D.
Direct Submission
Submitted (03-NOV-1999) P24, Robert Koch Institut, Nordufer
                                                                                                                                                                                                                      Viruges; 98DNA viruges; Circoviridae; Circovirus.

1 (bases 1 to 1768)

Mankertz,A., Domingo,M., Folch,J.M., LeCann,P., Jestin,A., Segales,J., Chmielewicz,B., Plana-Duran,J. and Soike,D. Characterisation of PCV-2 isolates from Spain, Germany and Virus Res. 66 (1), 65-77 (2000)
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/protein_id="AAF35297.1"
/db_xref="G1:7021351"
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mol type="genomic DNA"
isolate="GER3"
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2 isolate GER3,
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DB 14; Length 1768;

Score 1340; Pred. No. 0;

75.6**%**; 88.6**%**;

Query Match Best Local Similarity

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